

GenCore version 5.1.3
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OM nucleic - nucleic search, using SW model

Run on: February 3, 2003, 16:20:58 ; Search time 90 Seconds

(without alignments)
12878.925 Million cell updates/sec

Title: US-10-047-593-5

Perfect score: 2580

Sequence: 1.gcggccgcttaatacgactc.....cgctcttagaagggtcacgt 2580

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 396772 seqs, 224632407 residues

Total number of hits satisfying chosen parameters: 793544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications Na:*

1: /cggn2_6/ptodat/a//pubnra/US07_PUBCOMB.seq:*

2: /cggn2_6/ptodat/a/2/pubnra/PCT7_NEW_PUB.seq:*

3: /cggn2_6/ptodat/a/2/pubnra/US06_PUBCOMB.seq:*

4: /cggn2_6/ptodat/a/2/pubnra/US07_NEW_PUB.seq:*

5: /cggn2_6/ptodat/a/2/pubnra/US07_NEW_PUB.seq:*

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11: /cggn2_6/ptodat/a/2/pubnra/US10_NEW_PUB.seq:*

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13: /cggn2_6/ptodat/a/2/pubnra/US60_NEW_PUB.seq:*

14: /cggn2_6/ptodat/a/2/pubnra/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2579.6	100.0	2580	9 US-10-047-593-5
2	2579.6	100.0	7789	9 US-10-047-593-3
3	82.8	3.2	233	10 US-09-923-876-3107
4	68.6	2.7	12561	9 US-10-005-557A-41
5	66	2.6	281	10 US-9-923-876-4089
6	61.8	2.4	266	10 US-09-923-876-3931
7	46.4	1.8	305	10 US-0-864-761-19262
8	46.4	1.8	65158	9 US-09-771-208-20
9	46.2	1.8	299	10 US-09-864-761-21553
10	45.2	1.8	32195	10 US-09-764-870-111
11	45.2	1.8	32195	10 US-09-764-870-617
12	45.2	1.8	32195	10 US-09-764-869-1605
13	45	1.7	2580	9 US-10-047-593-5
14	45	1.7	7789	9 US-10-047-593-3
15	42.4	1.6	375	10 US-09-960-352-15014
16	41	1.6	479	10 US-09-864-761-3539
17	41	1.6	494	10 US-09-864-761-2947
18	40.8	1.6	726	10 US-09-864-761-19707
19	40.8	1.6	1951	10 US-09-864-761-2926

ALIGNMENTS

RESULT 1	US-10-047-593-5	Sequence 1	Appl
	; Sequence 5, Application US/10047593	Sequence 2	Appl
	; Patent No. US2002107094A1	Sequence 3	Appl
	; GENERAL INFORMATION:	Sequence 4	Appl
	; APPLICANT: Crane, Edmund H. III	Sequence 5	Appl
	; ATTORNEY: Rice, Douglas A.	Sequence 6	Appl
	; TITLE OF INVENTION: Maize NPRI Polynucleotides and Methods	Sequence 7	Appl
	; TITLE OF INVENTION: of Use	Sequence 8	Appl
	; CURRENT APPLICATION NUMBER: US/10/047-593	Sequence 9	Appl
	; CURRENT FILING DATE: 2002-01-15	Sequence 10	Appl
	; PRIOR APPLICATION NUMBER: 60/130,692	Sequence 11	Appl
	; PRIOR FILING DATE: 1999-04-23	Sequence 12	Appl
	; NUMBER OF SEQ ID NOS: 6	Sequence 13	Appl
	; SOFTWARE: FastSEQ for Windows Version 4.0	Sequence 14	Appl
	; SEQ ID NO: 5	Sequence 15	Appl
	; LENGTH: 2715	Sequence 16	Appl
	; TYPE: DNA	Sequence 17	Appl
	; ORGANISM: Zea mays	Sequence 18	Appl
	; FEATURE:	Sequence 19	Appl
	; NAME/KEY: promoter ^c	Sequence 20	Appl
	; LOCATION: (1)...(2715)	Sequence 21	Appl
	; Matches 2580; Conservative	Sequence 22	Appl
	; Best Local Similarity 100.0%; Score 2579.6; DB 9; Length 2580;	Sequence 23	Appl
	; Mismatches 0; Pred. No. 0; Indels 0; Gaps 0;	Sequence 24	Appl
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	Sequence 26	Sequence 27	Appl
	Sequence 28	Sequence 29	Appl
	Sequence 30	Sequence 31	Appl
	Sequence 32	Sequence 33	Appl
	Sequence 34	Sequence 35	Appl
	Sequence 36	Sequence 37	Appl
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	Sequence 112	Sequence 113	Appl
	Sequence 114	Sequence 115	Appl
	Sequence 116	Sequence 117	Appl
	Sequence 118	Sequence 119	Appl
	Sequence 120	Sequence 121	Appl

QY	181	GCGAGACCGTTGCCCGACGACGGTGCCTAACCGGA	CAGTCGGCACACAGCAGT	240	QY	1261	CTTCGTCATAAAGATCCATTACATTATTA	TACTGTCTATATACCTCA	1320
Db	181	GCAGACCTTGCCCCGACGACGGTGCCTAACCGGA	CAGTCGGCACACAGCAGT	240	Db	1261	CTTGTCCTATAAGATCCATTACATTATTA	TACTGTCTATATACCTCA	1320
QY	241	CCGGTGAATTATAGCCGTAACGCGCTTAATC	CTTCGGAGACGAGCAAGT	300	QY	1321	CTATCTGAGATCATCTGTTGGGAGCTAA	GGAGCTTGGGAGTTGGGTAAGCTAGA	1380
Db	241	CCGGTGAATTATAGCCGTAACGCGCTTAATC	CTTCGGAGACGAGCAAGT	300	Db	1321	CTATCTGAGATCATCTGTTGGGAGCTAA	GGAGCTTGGGAGTTGGGTAAGCTAGA	1380
QY	301	CAGCCTGGCAGCGGAACTGTCGGGAA	ACCCGACACTCCG	360	QY	1381	GCGACATGGGTCACAAACAAAC	ATGGGCAAGCTTGGGAA	1440
Db	301	CAGCCTGGCAGCGGAACTGTCGGGAA	ACCCGACACTCCG	360	Db	1381	GCGACATGGGTCACAAACAA	ATGGGCAACACACACTCACTA	1440
QY	361	AGCTGACTTTGGCTGAAAGTCATCTT	AGTCCTTCCAGT	420	QY	1441	ATTGGCTTCCAAATCGAGAGTCCCGT	AGAAGTACTCGTGTCTTGAG	1500
Db	361	AGCTGACTTTGGCTGAAAGTCATCTT	AGTCCTTCCAGT	420	Db	1441	ATTGGCTTCCAAATCGAGAGTCCCGT	AGAAGTACTCGTGTCTTGAG	1500
QY	421	ACTTAGACACATCATAGTCCTAA	ACATGTTAACTG	480	QY	1501	ATCAAATACCTCTTACAA	ATTTGTCATTTATTTGTCATTTA	1560
Db	421	ACTTAGACACATCATAGTCCTAA	ACATGTTAACTG	480	Db	1501	ATCAAATACCTCTTACAA	ATTTGTCATTTAAGCTAACAA	1560
QY	481	TACTTGGTTGACTTTGGCACCA	TTACACTTG	540	QY	1561	TCAAACTACCTCTTACAA	TTGTCATTTTGTGAAACATACCTTA	1560
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QY	541	ACCUAAACTTAAATGCGCC	AGGSCACATTCC	600	QY	1621	TRAGCTGACTGTTTTTG	GACCTTGACCATGCTG	1680
Db	541	ACCUAAACTTAAATGCGCC	AGGSCACATTCC	600	Db	1621	TRAGCTGACTGTTTTTG	GACCTTGACCATGCTG	1680
QY	601	GGGAAAGTCGGTACCTTGACT	CTTGTC	660	QY	1681	GTCGATGATTCATGG	ACGAACTGAGTTA	1740
Db	601	GGGAAAGTCGGTACCTTGACT	CTTGTC	660	Db	1681	GTCGATGATTCATGG	ACGAACTGAGTTA	1740
QY	661	CTATAGCGTTTGAGTCGAC	GGCGTGGCG	720	QY	1741	TTCACACGTGTTG	ACGGGTTAGGAA	1740
Db	661	CTATAGCGTTTGAGTCGAC	GGCGTGGCG	720	Db	1741	TTCACACGTGTTG	ACGGGTTAGGAA	1740
QY	721	GACAGTCGGTGAATTATACGGG	AGCGCCCTCG	780	QY	1801	GTGAGGTTGTTACGTT	TTAGGATTA	1860
Db	721	GACAGTCGGTGAATTATACGGG	AGCGCCCTCG	780	Db	1801	GTGAGGTTGTTACGTT	TTAGGATTA	1860
QY	781	GGGSCGCTGCTGCGCA	AAATCAGCAGCA	840	QY	1861	CATAACTCTAGTC	TTTTAATGAGCT	1920
Db	781	GGGSCGCTGCTGCGCA	AAATCAGCAGCA	840	Db	1861	CATAACTCTAGTC	TTTTAATGAGCT	1920
QY	841	CCTTCCTCTATTATGTCGCTA	TGGTTGTTGTTG	900	QY	1921	GTACAGAAACATG	ACGATTTGAA	1980
Db	841	CCTTCCTCTATTATGTCGCTA	TGGTTGTTGTTG	900	Db	1921	GTACAGAAACATG	ACGATTTGAA	1980
QY	901	TATGCACTGTGAGATA	ATCACATAGCA	960	QY	1981	TGGGACCGTACAGA	CTAGAGGATAGGAGG	2040
Db	901	TATGCACTGTGAGATA	ATCACATAGCA	960	Db	1981	TGGGACCGTACAGA	CTAGAGGATAGGAGG	2040
QY	961	CGTCACTAAATCTATTATG	AAGTGGT	1020	QY	2041	GGGGTCACGTCACCC	CTGGTCACTGAGCT	2100
Db	961	CGTCACTAAATCTATTATG	AAGTGGT	1020	Db	2041	GGGGTCACGTCACCC	CTGGTCACTGAGCT	2100
QY	1021	CTATAGCTGCTGAGCTCTG	CACTGAGCT	1080	QY	2101	GGTTTCTTCAATTCGCGGA	AACTCTGAGCTT	2160
Db	1021	CTATAGCTGCTGAGCTCTG	CACTGAGCT	1080	Db	2101	GGTTTCTTCAATTCGCGGA	AACTCTGAGCTT	2160
QY	1081	GGTCCTCGACATGCGAGAC	CTAGGGCT	1140	QY	2161	TCAATCTCTCGG	GGCCCTCTGAGCT	2220
Db	1081	GGTCCTCGACATGCGAGAC	CTAGGGCT	1140	Db	2161	TCAATCTCTCGG	GGCCCTCTGAGCT	2220
QY	1141	GGCTCTAGATGCGACTG	AGCTGCGCT	1200	QY	2221	TTCGATCCACTCTT	CCGCGCTCTGCGCC	2280
Db	1141	GGCTCTAGATGCGACTG	AGCTGCGCT	1200	Db	2221	TTCGATCCACTCTT	CCGCGCTCTGCGCC	2280
QY	1201	TGTTTGGCAACTCTG	ATGCTGTTG	1260	QY	2281	GGACTCTTCG	CGGCTCTGCGCC	2340
Db	1201	TGTTTGGCAACTCTG	ATGCTGTTG	1260	Db	2281	GGACTCTTCG	CGGCTCTGCGCC	2340
QY	1261	CCAGCACCACACCTCC	ACCGTT	1280	QY	2341	CCAGCACCACACCTCC	ACCGTT	1280

RESULT²
US-10-047-593-3
Sequence 3, Application US/10047593
Patent No. US2002170094A1
GENERAL INFORMATION:
APPLICANT: Crane, Edmund H. III
APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Maize NPRI Polynucleotides and Methods
TITLE OF INVENTION: of Use
FILE REFERENCE: 1090D2
CURRENT APPLICATION NUMBER: US/10/047, 593
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/1130, 692
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: 09/551,778
PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 7789
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: promoter
LOCATION: (1...)(2715)
NAME/KEY: 5'UTR
LOCATION: (2716)...(2781)
NAME/KEY: exon
LOCATION: (2782)...(3435)
LOCATION: (3336)...(3987)
NAME/KEY: exon
LOCATION: (3988)...(4738)
NAME/KEY: intron
LOCATION: (4739)...(5274)
NAME/KEY: exon
LOCATION: (5275)...(5475)
NAME/KEY: intron
LOCATION: (5476)...(5665)
NAME/KEY: exon
LOCATION: (5666)...(5922)
LOCATION: (5926)...(6124)
US-10-047-593-3

Query Match 100.0%; Score 2579.6; DB 9; Length 7789;
Best Local Similarity 100.0%; Pred. No. 0; Matches 2580; Conservative 0; Mismatches 0; Index 0; Gaps 0;

Qy 1 GCGGCCGCGTAACTACACTCACTATAGGGGAAGATTCCGATCCTTCCTTAATTCGC 60
Db 1 GCGGCCGCGTAACTACACTCACTATAGGGGAAGATTCCGATCCTTCCTTAATTCGC 60
Qy 61 GAAGCGGACCTTGCGCTTGGAGCGCGACCTGCGTCAACCG 120
Db 61 GAAGCGGACCTTGCGCTTGGAGCGCGACCTGCGTCAACCG 120

Qy 2461 CATATTTCTGTCTGCTGAGCTGATGATTAGCCACCG 2520
Db 2461 CATATTTCTGTCTGCTGAGCTGATGATTAGCCACCG 2520
Qy 2521 GCTGGAGACTCCGTGATTTAGCGGACTTCCGCCCTCTAGGAAGGGTCAGT 2580
Db 2521 GCTGGAGACTCCGTGATTTAGCGGACTTCCGCCCTCTAGGAAGGGTCAGT 2580

Qy 121 GACAGTCAGGTGCCCTTCGACGGTGGCTCSCCACGCTGTTTCGCGGATCGCG 180
Db 121 GACAGTCAGGTGCCCTTCGACGGTGGCTCSCCACGCTGTTTCGCGGATCGCG 180
Qy 181 GCAGACGGTGGCCGACCCACCGTGGCTACCGGACGCTGGTGCACCCGACGT 240
Db 181 GCAGACGGTGGCCGACCCACCGTGGCTACCGGACGCTGGTGCACCCGACGT 240
Qy 241 CGGCGAATTTAGCGTAGCCGTTAATCTCCGAGAGCAGTCGGTACCGAAC 240
Db 241 CGGCGAATTTAGCGTAGCCGTTAATCTCCGAGAGCAGTCGGTACCGAAC 240
Qy 301 CAGCCCTGGCACCGACACTGTCGGTAACTCACTCCGAGAGCAGTCGGTACCG 360
Db 301 CAGCCCTGGCACCGACACTGTCGGTAACTCACTCCGAGAGCAGTCGGTACCG 360
Qy 361 AGCTGACTTGTGCTGACAGTCATTTAGTCTCAACTTGTGTTCTGTTCCAGC 420
Db 361 AGCTGACTTGTGCTGACAGTCATTTAGTCTCAACTTGTGTTCTGTTCCAGC 420
Qy 421 ACTTAGACACATACATTAGTCTTAAACACATGTTAATCTGAGAACATACCTTA 480
Db 421 ACTTAGACACATACATTAGTCTTAAACACATGTTAATCTGAGAACATACCTTA 480
Qy 481 TACTGGTTGACTTGTCCACATTACACTGGGACTGTGTTGGACACTAATTC 540
Db 481 TACTGGTTGACTTGTCCACATTACACTGGGACTGTGTTGGACACTAATTC 540
Qy 541 ACCAAATACTTAAATGCCCCAGGGACATTCCCTTACAGTCGGACAC 600
Db 541 ACCAAATACTTAAATGCCCCAGGGACATTCCCTTACAGTCGGACAC 600
Qy 601 CGGACAGTCGGTACCTCTGACTCTGCTGTTAATCTGCGGACTGTGTTGCA 660
Db 601 CGGACAGTCGGTACCTCTGACTCTGCTGCGGACTGTGTTGCA 660
Qy 661 CTATAGCGTTTGCAGTGACCTTGGGACACTGGCTCGCTCGCTGACCG 720
Db 661 CTATAGCGTTTGCAGTGACCTTGGGACACTGGCTCGCTCGCTGACCG 720
Qy 721 GACAGTCGATGATTATAGCGGASCGGCCCTGTGAATTCCGAGTGTGGCTGTGAA 780
Db 721 GACAGTCGATGATTATAGCGGASCGGCCCTGTGAATTCCGAGTGTGGCTGTGAA 780
Qy 781 GGCGCCCTGGCTGTGACCGACAACTGATGTTGGCCAAATTCGACACTAAGT 840
Db 781 GGCGCCCTGGCTGTGACCGACAACTGATGTTGGCCAAATTCGACACTAAGT 840
Qy 841 CCTTGTGCTTCAATTATGGTGTGCTAACTGGATCTTGTGTTGGTGAACCT 900
Db 841 CCTTGTGCTTCAATTATGGTGTGCTAACTGGATCTTGTGTTGGTGAACCT 900
Qy 901 TATGCCACTTGAATAATCACCTCTGCCAACACTAGTGGCCAAATTCGACACTAAGT 960
Db 901 TATGCCACTTGAATAATCACCTCTGCCAACACTAGTGGCCAAATTCGACACTAAGT 960
Qy 961 CGTCAACTAACTTATAGAAAGTGTACCCAAACTAGTGGCCAAATTCGACACTAAGT 1020
Db 961 CGTCAACTAACTTATAGAAAGTGTACCCAAACTAGTGGCCAAATTCGACACTAAGT 1020
Qy 1021 CTATAGCTGAGATAATCACCTCTGCCAACACTAGTGGCCAAATTCGACACTAAGT 1080
Db 1021 CTATAGCTGAGATAATCACCTCTGCCAACACTAGTGGCCAAATTCGACACTAAGT 1080
Qy 1081 GTCCTGACATGCGACCTAGGCCCGTTAGATGGCTTCCTTCAGACACT 1140
Db 1081 GTCCTGACATGCGACCTAGGCCCGTTAGATGGCTTCCTTCAGACACT 1140
Qy 1141 GCTCTAGATGCTGAGACTGCTGCGTCTTAATAGTATGATGA 1200
Db 1141 GCTCTAGATGCTGAGACTGCTGCGTCTTAATAGTATGATGA 1200
Qy 1201 TGTTCACATGATGATGCTGCTTACAAAGCTGTTTACTC 1260

APPLICANT: Mahajan, Pramod ; SEQ ID NO: 4089
 APPLICANT: Rafalki, Antoni J. ; LENGTH: 281
 APPLICANT: Sakai, Hajime ; TYPE: DNA
 APPLICANT: Klein, Ted M. ; ORGANISM: Zea mays
 TITLE OF INVENTION: Transcriptional Regulator Nucleic Acids, ; FEATURE:
 FILE REFERENCE: 1288 ; NAME/KEY: misc feature
 CURRENT APPLICATION NUMBER: US/10/005, 057A ; OTHER INFORMATION: Incyte ID No. US20020013958A1 700454406H1
 CURRENT FILING DATE: 2001-12-04 ; SEQ ID NO: 41
 PRIOR APPLICATION NUMBER: 60/251, 555
 NUMBER OF SEQ ID NOS: 41 ; LENGTH: 12561
 SEQ ID NO: 41 ; TYPE: DNA
 LENGTH: 12561
 ORGANISM: zea mays
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Zmpk1 genomic sequence
 LOCATION: (1)..(12561)
 OTHER INFORMATION: Name/Key: misc feature
 LOCATION: (1)..(12561)
 OTHER INFORMATION: N = A,T,C or G
 US-10-005-057A-41

Query Match 2.7%; Score 68.6; DB 9; Length 12561;
 Best Local Similarity 56.2%; Pred. No. 9.6e-08; Matches 187; Conservative 1; Mismatches 140; Indels 5; Gaps 3;

Qy 717 ACCGACAGCTCCGATGAAATTAGGGGATGGCTGTGAATTCGGAGTGGCTGTT 776
 Db 12396 ACCGACAGCTCCGATGAAATTAGGGGATGGCTGTGAATTCGGAGTGGCTGTT 12337

Qy 777 TGAAGGCCGCGCTGGCGTGCACGCAACGATGATGCTGCGCCAAATTAGCACA 836
 Db 12336 TG-AGTTGAGCTCTCTGGACCGACAGTCGGTCCCCAACGAGKGTGCTTC 12278

Qy 837 AAGTGTCTTGCTTAATTATTGTTGCTGCTAACCTGGATTCTTGTGTTGCTGTA 896
 Db 12277 GGTTGTCTTGCTGCTAACCTGGATTCTTGTGTTGCTGTA 12218

Qy 897 ACCTATGACTG-AGTAAATCACCTGACCAACTGATGTCAGTGGTTG 955
 Db 12217 ACCTTGTACACCTGTTAATTCTGATCTGGCAAAATTAGTATTCCTTATTGTG 12158

Qy 956 TTGATCGTCAACTAAATCTATTTATAG--AAAGTGGTTAACCTTATTCCCTTC 1012
 Db 12157 TGGCAATTCAACCACCAAAATTATAGGACTATAGGTTAACCTTATTCCCTTC 12098

Qy 1013 AGCAACTCTATACTGCTGAGACTGCTGAC 1045
 Db 12097 ATCTCCCTTTGGTGGATGATGCCAACACA 12065

RESULT 6
 Sequence 3931, application US/09923876
 Patent No. US20020013958A1
 GENERAL INFORMATION:
 APPLICANT: Lalgudi, Raghunath V.
 APPLICANT: Kamigaki, Laura Y. (Ito)
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
 FILE REFERENCE: PL-0012-1 CON
 CURRENT APPLICATION NUMBER: US/09/923, 876
 CURRENT FILING DATE: 2001-08-06
 PRIOR APPLICATION NUMBER: 09/298, 329
 PRIOR FILING DATE: 1999-04-21
 PRIOR APPLICATION NUMBER: 60/1085, 331
 PRIOR FILING DATE: 1998-05-05
 NUMBER OF SEQ ID NOS: 6332
 SOFTWARE: PERL Program
 SEQ ID NO: 3931
 LENGTH: 266
 TYPE: DNA
 ORGANISM: zea mays
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. US20020013958A1 700454106H1
 NAME/KEY: unsure
 LOCATION: 201, 211, 234, 244-245
 OTHER INFORMATION: a, t, c, g, or other
 US-09-923-876-3931

Query Match 2.4%; Score 61.8; DB 10; Length 266;
 Best Local Similarity 84.6%; Pred. No. 7.5e-07; Matches 66; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

US-09-923-876-4089/c

Sequence 4089, Application US/09923876

Patent No. US20020013958A1

GENERAL INFORMATION:

APPLICANT: Lalgudi, Raghunath V.

APPLICANT: Kamigaki, Laura Y. (Ito)

APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING

FILE REFERENCE: PL-0012-1 CON

CURRENT APPLICATION NUMBER: US/09/923, 876

CURRENT FILING DATE: 2001-08-05

PRIOR APPLICATION NUMBER: 09/298, 329

PRIOR FILING DATE: 1998-04-21

PRIOR APPLICATION NUMBER: 60/1085, 331

NUMBER OF SEQ ID NOS: 6332

SOFTWARE: PERL Program

RESULT 7
 Sequence 1962, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharron G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.

PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 09/551,778
; PRIOR FILING DATE: 2000-04-18
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 7789
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE: promoter
; LOCATION: (1)...(2715)
; NAME/KEY: 5'UTR
; LOCATION: (2716)...(2781)
; NAME/KEY: exon
; LOCATION: (2782)...(3435)
; NAME/KEY: intron
; LOCATION: (3436)...(3987)
; NAME/KEY: exon
; LOCATION: (3988)...(4738)
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; LOCATION: (4739)...(5274)
; NAME/KEY: exon
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; LOCATION: (5476)...(5665)
; NAME/KEY: exon
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; NAME/KEY: 3'UTR
; LOCATION: (5926)...(6124)
; US-10-047-593-3

RESULT 15
Query Match Similarity 1.7%; Score 45; DB 9; Length 7789;
Best Local Similarity 54.5%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

Qy 188 GTTGGCCCGACCGACCTTGCTTCAACGGAGACTCGGTGACACAGAAGTCGGTGA 247
Db 352 GTCGACCGAGCTGTCGGTCAACGGAGCTGTCGGTGCAGGTGGCTCAGG 293
Qy 248 ATTATAGCCGTACGCCCTTAATCACTTCGGAGAGAAGCTGGCTGAGCCGCTG 307
Db 292 GAACTTGCTGCTCGGAAGCTGATAACCGGTAGGGTAAATCACCGACTGTC 233
Qy 308 GGGCACCGGACACTGTCGGTGAAACCCACCGGACAGCGGACGCGGAC 352
Db 232 GTCGACCGGACTGTCGGTGAGCCACGGTCGGCAAC 188

US-09-960-352-15014/C
; Sequence 15014, Application US/03960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21.102981C
; CURRENT APPLICATION NUMBER: US09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 15014
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 64-LIB305B-048-01-KL-H8
; US-09-960-352-15014
Query Match Similarity 1.6%; Score 42.4; DB 10; Length 375;
Best Local Similarity 51.0%; Pred. No. 0.13;

